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Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2008; month=4; day=25; hr=15; min=56; sec=41; ms=329;]

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Reviewer Comments:

For SEQ ID # 40 through 45 and 48 through 53, numeric identifier <213> can only be one of three choices, "Scientific name, i.e. Genus/species, Unknown or Artificial Sequence."

Application No: 10585149 Version No: 1.0

Input Set:

Output Set:

Started: 2008-04-09 18:38:03.989
Finished: 2008-04-09 18:38:06.159
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 170 ms
Total Warnings: 46
Total Errors: 0
No. of SeqIDs Defined: 53
Actual SeqID Count: 53

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)

Input Set:

Output Set:

Started: 2008-04-09 18:38:03.989
Finished: 2008-04-09 18:38:06.159
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 170 ms
Total Warnings: 46
Total Errors: 0
No. of SeqIDs Defined: 53
Actual SeqID Count: 53

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (30) This error has occurred more than 20 times, will not be displayed
W 402	Undefined organism found in <213> in SEQ ID (40)
W 402	Undefined organism found in <213> in SEQ ID (41)
W 402	Undefined organism found in <213> in SEQ ID (42)
W 402	Undefined organism found in <213> in SEQ ID (43)
W 402	Undefined organism found in <213> in SEQ ID (44)
W 402	Undefined organism found in <213> in SEQ ID (45)
W 402	Undefined organism found in <213> in SEQ ID (48)
W 402	Undefined organism found in <213> in SEQ ID (49)
W 402	Undefined organism found in <213> in SEQ ID (50)
W 402	Undefined organism found in <213> in SEQ ID (51)
W 402	Undefined organism found in <213> in SEQ ID (52)
W 402	Undefined organism found in <213> in SEQ ID (53)

SEQUENCE LISTING

<110> KaloBios, Inc.

Bebbington, Christopher Robert
Yu, Bo

<120> Transactivation System for Mammalian
Cells

<130> 73678-023

<140> 10585149

<141> 2008-04-09

<150> 04815827.3

<151> 2006-02-21

<150> US 60/533,917

<151> 2003-12-31

<160> 53

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 236

<212> PRT

<213> Hamster

<400> 1

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Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Val
20 25 30

Gly Asp Val Asp Ala Ala Pro Leu Gly Ala Ala Pro Thr Pro Gly Ile
35 40 45

Phe Ser Phe Gln Pro Glu Ser Asn Pro Thr Pro Ala Val His Arg Asp
50 55 60

Met Ala Ala Arg Thr Ser Pro Leu Arg Pro Ile Val Ala Thr Thr Gly
65 70 75 80

Pro Thr Leu Ser Pro Val Pro Pro Val Val His Leu Thr Leu Arg Arg
85 90 95

Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Arg Asp Phe Ala Glu Met
100 105 110

Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly Arg Phe Ala
115 120 125

Thr Val Val Glu Leu Phe Arg Asp Gly Val Asn Trp Gly Arg Ile
130 135 140

Val Ala Phe Phe Glu Phe Gly Val Met Cys Val Glu Ser Val Asn
145 150 155 160

Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp Met Thr Glu
165 170 175

Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn Gly Gly Trp
180 185 190

Asp Ala Phe Val Glu Leu Tyr Gly Pro Ser Val Arg Pro Leu Phe Asp
195 200 205

Phe Ser Trp Leu Ser Leu Lys Thr Leu Leu Ser Leu Ala Leu Val Gly
 210 215 220
 Ala Cys Ile Thr Leu Gly Thr Tyr Leu Gly His Lys
 225 230 235

<210> 2
 <211> 195
 <212> PRT
 <213> hamster

<400> 2

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 20 25 30
 Gly Asp Val Asp Ala Ala Ala Ala Ala Ser Pro Val Pro Pro Val
 35 40 45
 Val His Leu Thr Leu Arg Arg Ala Gly Asp Asp Phe Ser Arg Arg Tyr
 50 55 60
 Arg Arg Asp Phe Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe
 65 70 75 80
 Thr Ala Arg Gly Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp
 85 90 95
 Gly Val Asn Trp Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val
 100 105 110
 Met Cys Val Glu Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn
 115 120 125
 Ile Ala Leu Trp Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp
 130 135 140
 Ile Gln Asp Asn Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly Pro
 145 150 155 160
 Ser Val Arg Pro Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr Leu
 165 170 175
 Leu Ser Leu Ala Leu Val Gly Ala Cys Ile Thr Leu Gly Thr Tyr Leu
 180 185 190
 Gly His Lys
 195

<210> 3
 <211> 588
 <212> DNA
 <213> hamster

<400> 3

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 gccgcgagcc ccgtgccacc tgggtccac ctgaccctcc gccgggctgg ggatgacttc 180
 tccccgtcgct accgtcgca cttcgccggag atgtccagtc agctgcaccc gacgccttc 240
 accgcgaggg gacgcattgc tacgggtggg gaggaactct tcagggatgg ggtgaactgg 300
 gggaggattg tggccttctt tgagttcggt ggggtcatgt gtgtggagag cgtcaacagg 360
 gagatgtcac ccctgtgga caacatcgcc ctgtggatga ccgagttaccc gaaccggcat 420
 ctgcacaccc ggatccagga taacggaggc tgggacgcatttggaaact gtacggcccc 480
 agtgtgaggc ctctgtttga tttcttgg ctgtctctga agacccctgct cagcctggcc 540
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<210> 4
 <211> 289

<212> PRT

<213> Human adenovirus type 5

<400> 4

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1 5 10 15
Ala Ser Leu Leu Asp Gln Leu Ile Glu Glu Val Leu Ala Asp Asn Leu
20 25 30
Pro Pro Pro Ser His Phe Glu Pro Pro Thr Leu His Glu Leu His Asp
35 40 45
Leu Asp Val Thr Ala Pro Glu Asp Pro Asn Glu Glu Ala Val Ser Gln
50 55 60
Ile Phe Pro Asp Ser Val Met Leu Ala Val Gln Glu Gly Ile Asp Leu
65 70 75 80
Leu Thr Phe Pro Pro Ala Pro Gly Ser Pro Glu Pro Pro His Leu Ser
85 90 95
Arg Gln Pro Glu Gln Pro Glu Gln Arg Ala Leu Gly Pro Val Ser Met
100 105 110
Pro Asn Leu Val Pro Glu Val Ile Asp Leu Thr Gly His Glu Ala Gly
115 120 125
Phe Pro Pro Ser Asp Asp Glu Asp Glu Glu Gly Glu Glu Phe Val Leu
130 135 140
Asp Tyr Val Glu His Pro Gly His Gly Cys Arg Ser Cys His Tyr His
145 150 155 160
Arg Arg Asn Thr Gly Asp Pro Asp Ile Met Cys Ser Leu Cys Tyr Met
165 170 175
Arg Thr Cys Gly Met Phe Val Tyr Ser Pro Val Ser Glu Pro Glu Pro
180 185 190
Glu Pro Glu Pro Glu Pro Glu Pro Ala Arg Pro Thr Arg Arg Pro Lys
195 200 205
Met Ala Pro Ala Ile Leu Arg Arg Pro Thr Ser Pro Val Ser Arg Glu
210 215 220
Cys Asn Ser Ser Thr Asp Ser Cys Asp Ser Gly Pro Ser Asn Thr Pro
225 230 235 240
Pro Glu Ile His Pro Val Val Pro Leu Cys Pro Ile Lys Pro Val Ala
245 250 255
Val Arg Val Gly Gly Arg Arg Gln Ala Val Glu Cys Ile Glu Asp Leu
260 265 270
Leu Asn Glu Pro Gly Gln Pro Leu Asp Leu Ser Cys Lys Arg Pro Arg
275 280 285
Pro

<210> 5

<211> 986

<212> DNA

<213> Human adenovirus type 5

<400> 5

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cctacccttc acgaactgca tgattttagac gtgacggccc ccgaagatcc caacgaggag 180
gcgggttcgc agattttcc cgactctgtat atgttggcgg tgcatggagg gattgactta 240
ctcaactttc cgccggcgcc cgggtctccg gagccgcctc acctttcccg gcagcccgag 300
cagccggagc agagagcctt gggtccgggtt tctatgccaa accttgcatttccggatc 360
gatcttaccg gccacgaggc tggctttcca cccagtgcacg acgaggatga agagggtgag 420
gagtttgcgt tagattatgt ggagcacccc gggcacgggtt gcaggtcttgcattatcac 480

cgaggagaata	cgggggaccc	agatattatg	tgttcgctt	qctatatgag	gacctgtggc	540
atgtttgtct	acagtaagtg	aaaattatgg	gcagtggtg	atagagtgt	gggttggtg	600
tggtaatttt	tttttaatt	tttacagttt	tgtggttaa	agaattttgt	attgtgattt	660
ttttaaaagg	tcctgtgtct	gaacctgagc	ctgagcccg	gccagaaccg	gagccctgcaa	720
gacctacccg	ccgtccctaa	atggcgctg	ctatcctgag	acgcccggaca	tcacctgtgt	780
ctagagaatg	caatagtagt	acggatagct	gtgactccgg	tccttctaac	acaccccttg	840
agatacaccc	ggtggtcccg	ctgtgcccc	ttaaaccagt	tgccgtgaga	gttgggtggc	900
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tgagctgtaa	acgccccagg	ccataaa				986

<210> 6
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 6
cccgaaatcg ccggccaccat gggacatatt atctggccac 39

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<210> 7
<211> 28
<212> DNA
<213> Artificial Sequence
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<220>
<223> primer

<400> 7
cccatcgacc ttatggatg gggcattt 28

<210> 8
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<210> 9
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<233> primary

<210> 10
<211> 25
<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 10
ggaggtgatc gatcttaccg gccac 25

<210> 11
<211> 36
<212> DNA
<213> Artificial Sequence

<220>

<223> primer

<400> 11
cctacccttc acgaactgca tgat tagac gtgacg 36

<210> 12
<211> 36
<212> DNA
<213> Artificial Sequence

<220>

<223> primer

<400> 12
cgtcacgtct aaatcatgca gttcgtgaag ggtagg 36

<210> 13
<211> 38
<212> DNA
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<223> primer

<400> 13
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<210> 14
<211> 29
<212> DNA
<213> Artificial Sequence

<220>

<223> primer

<400> 14
cccggtcgacc aacattcatt cccgagggt 29

<210> 15
<211> 558
<212> DNA
<213> Human adenovirus type 5

<400> 15

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caggcaaaagt tagtctgcag aattaaggag gattacaagt gggaaatttga agagctttg      180
aaatcctgtg gtgagctgtt tgattcttg aatctgggtc accaggcgct tttccaagag      240
aaggcatca agacttggg ttttccaca cggggcgcg ctgcggctgc tgggttttt      300
ttgagttta taaaggataa atggagcgaa gaaaccatc tgacgggggg gtacctgctg      360
gatttctgg ccatgcacatct gtggagagcg gttgtgagac acaagaatcg cctgctactg      420
ttgtcttccg tccgcccggc gataataccg acggaggagc agcagcagca gcaggagggaa      480
gccaggcgcc ggcggcagga gcagagccca tggaaaccga gagccggct ggaccctcg      540
gaatgaatgt tggcgac                                558
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<210> 16

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 16

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cccggtcgacg ccgcaccat gcccggccaaa acccccccg                                38
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<210> 17

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 17

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<210> 18

<211> 2824

<212> DNA

<213> Homo sapiens

<400> 18

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gacagcggcc cggaggaccc gcctctcgtc aggcttgagt ttgaagaaac agaagaacct      180
gattttactg cattatgtca gaaattaaag ataccagatc atgtcagaga gagagcttgg      240
ttaacttggg agaaagtttc atctgtggat ggagtattgg gaggttatat tcaaaagaaa      300
aaggaactgt ggggaatctg tatcttttgc acacgagttg acctagatga gatgtcggttc      360
actttactga gctacagaaa aacatacgaa atcagtgatc ataaattctt taacttacta      420
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gatgtattgt ttgcacttctt cagcaatttg gaaaggacat gtgaacttat atatttgcaca      540
caacccagca gttcgatatac tactgaaata aattctgtat tgggtctaaa agtttcttgg      600
atcacatttt tattagctaa aggggaagta ttacaatgg aagatgtatct ggtgatttca      660
tttcagttaa tgctatgtgt ccttgactat tttttaaaatcttccatgttgcgtc      720
aaagaaccat ataaaacacgc tggatatacc attaatgttt cacctcgaaac acccaggcgaa      780
ggtcagaaca ggagtgcacg gatagcaaaa caactagaaa atgatacaag aattattgaa      840
gttctctgtt aagaacatgtt atgtaatata gatgaggtgtt aaaaatgtttt tttcaaaaat      900
tttataccctt ttatgtatcc tcttggactt gtaacatcta atggacttcc agaggttggaa      960
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aggactgtta tgaacactat ccaacaatta atgatgattt taaattctgc aagtgtcaaa	1200
cttcagaaa atctgatttc ctatTTtaac aactgcacag tgaatccaaa agaaagtata	1260
ctgaaaagag tgaaggatatac tttaaagaga aatttgctaa agctgtggga	1320
cagggttgtg tcgaaattgg atcacagcga tacaaactt gaggTCGCTT gtattaccga	1380
gtaatggaat ccatgcttaa atcagaagaa gaacgattat ccattcaaaa ttttagcaaa	1440
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gccacatata gcagaagtac atctcagaat cttgattctg gaacagattt gtcttccc	1560
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tcaaaggacc gagaaggacc aactgatcac cttgaatctg cttgtccct taatcttcc	1800
ctccagaata atcacactgc agcagatattat tattttctc ctgtaaagatc tccaaagaaa	1860
aaaggTTcaa ctacgcgtgt aaattctact gcaaatgcag agacacaagc aacctcagcc	1920
ttccagaccc agaaggcatt gaaatctacc tctcttcaac tttttataa aaaagtgtat	1980
cggctagcct atctccggct aaatacactt tgtgaacgccc ttctgtctga gcacccagaa	2040
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agagacagggc atttggacca aattatgatg tttccatgt atggcatatg caaagtgaag	2160
aatatagacc ttaaattcaa aatcattgt aacgcataca aggcatttcc tcatgctgtt	2220
caggagacat tcaaacgtgt ttgtatcaaa gaagaggagt atgattctat tatagtattc	2280
tataactcg tcttcatgca gagactgaaa acaaataattt tgcagttatgc ttccaccagg	2340
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cccttacgga ttccctggagg gaacatctat atttcccc tgaagagtcc atataaaattt	2460
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ggtgaatcat tcgggacttc tgagaagttc cagaaaataa atcagatggt atgtacagc	2580
gaccgtgtgc tcaaagaag tgctgaagga agcaacccctc ctaaaaccact gaaaaaacta	2640
cgcttgcata ttgaaggatc agatgaagca gatggaagta aacatctccc aggagagtcc	2700
aaatttcagc agaaactggc agaaatgact tctactcgaa cacgaatgca aaagcagaaa	2760
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ccgc	2824

<210> 19

<211> 928

<212> PRT

<213> Homo sapiens

<400> 19

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20	25	30	
Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg Leu Glu			
35	40	45	
Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln Lys Leu			
50	55	60	
Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp Glu Lys			
65	70	75	80
Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys Lys Lys			
85	90	95	
Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Arg Val Asp Leu Asp Glu			
100	105	110	
Met Ser Phe Thr Leu Leu Ser Tyr Arg Lys Thr Tyr Glu Ile Ser Val			
115	120	125	
His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr Lys Val			
130	135	140	
Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe Ala			

145	150	155	160
Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu	Leu Ile Tyr Leu Thr Gln		
165	170	175	
Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala	Leu Val Leu Lys		
180	185	190	
Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly	Glu Val Leu Gln Met		
195	200	205	
Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met	Leu Cys Val Leu Asp		
210	215	220	
Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu	Lys Glu Pro Tyr Lys		
225	230	235	240
Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg	Thr Pro Arg Arg Gly		
245	250	255	
Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu	Glu Asn Asp Thr Arg		
260	265	270	
Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys	Asn Ile Asp Glu Val		
275	280	285	
Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe	Met Asn Ser Leu Gly		
290	295	300	
Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu	Asn Leu Ser Lys Arg		
305	310	315	320
Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp	Leu Asp Arg Arg Leu Phe		
325	330	335	
Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser	Ile Asp Ser Phe Glu		
340	345	350	
Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp	Glu Val Glu Val Asn Ile		
355	360	365	
Ile Pro Pro His Thr Pro Val Arg Thr Val Met	Asn Thr Ile Gln Gln		
370	375	380	
Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln	Pro Ser Glu Asn Leu		
385	390	395	400
Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro	Lys Glu Ser Ile Leu		
405	410		